

Chromosomal locus	Description	ESTs	Paralog	ParaESTs	Bit Score	E Value	Identities
Redundant paralogs:							
At2g18450	succinate dehydrogenase flavoprotein subunit	2	At5g66760	40	1112	0.0	84%
At2g40800	unknown protein	4	At3g56430	2	559	e-159	73%
At3g05780	Lon protease	0	At5g26860	17	1187	0.0	67%
At3g12110	actin (ACT11)	20	At5g09810	161	736	0.0	95%
At3g46520	actin (ACT12)	3	At5g09810	161	712	0.0	92%
At5g59370	actin (ACT4)	2	At5g09810	161	711	0.0	92%
At3g16480	mitochondrial processing peptidase alpha	17	At1g51980	25	741	0.0	74%
At3g27620	alternative oxidase (AOX1c)	2	At3g22370	18	497	e-141	87%
At4g23900	nucleotide diphosphate kinase III	4	At4g11010	17	402	e-113	82%
At4g35650	isocitrate dehydrogenase subunit I	2	At4g35260	21	558	e-159	76%
At1g55860	ubiquitin-protein ligase 2 (UPL2)	18	At1g70320	15	6026	0.0	84%
At3g60100	citrate synthase	1	At2g44350	10	720	0.0	83%
At4g24190	HSP 90 related	73	At2g04030	31	560	e-159	43%
At5g50920 [#]	Clp protease ATP binding subunit	48	At3g48870	14	1422	0.0	83%
At4g35090 [#]	catalase 2	99	At4g35090	29	935	0.0	86%
Paralogs with a unique peptide at low confidence:							
At1g07510	AAA-type ATPase	10	At2g29080	22	1202	0.00	77%
At1g56190	phosphoglycerate kinase	19	At3g12780	130	758	0.0	86%
At3g20040	hexokinase 2	0	At1g50460	7	653	0.0	75%
At3g22360	alternative oxidase (AOX1b)	3	At3g22370	18	507	e-144	76%
At3g19480	D-3-phosphoglycerate dehydrogenase	6	At4g34200	30	688	0.0	80%
At3g10270	DNA gyrase subunit B	1	At5g04130	8	1061	0.0	82%
At4g28390	adenosine nucleotide translocator	4	At5g13490	20	513	e-146	68%
At4g37930	glycine hydroxymethyltransferase	167	At5g26780	9	880	0.0	85%
At5g14300	prohibitin	1	At5g40770	10	311	2e-85	63%
At4g28620	ABC transporter	2	At5g58270	7	930	0.0	70%
At5g64990	GTP-binding protein	1	At2g22290	1	295	9e-81	76%

Indistinguishable paralogs:

At5g60390	elongation factor 1 alpha (EF1-alpha)	579	At1g07940	121	878	0.0	100%
			At1g07930	141	878	0.0	100%
			At1g07920	155	878	0.0	100%
At5g08670	ATP synthase beta subunit (ATP2)	103	At5g08690	66	992	0.0	96%
			At5g08680	70	974	0.0	95%

Supplementary Table 2. Redundant or homologous proteins from the set of 416.

The redundant paralogs are proteins that do not have supporting MS data to be positively included in the final set but nonetheless fulfilled the matching criteria for initial inclusion. These proteins were excluded from further analyses. Paralogs with a unique peptide at low confidence were successfully identified by MS but the peptide that differentiated the protein from its closest homolog was matched at low confidence (ProID confidence score < 98). These proteins were excluded from further analyses. Indistinguishable paralogs are those proteins that cannot be distinguished from each other based on mass spectrometric data obtained in this analysis; these proteins have been included in further analyses. ESTs, expressed sequence tags of redundant paralog; Paralog, the protein that was unable to be distinguished from by MS; ParaESTs, expressed sequence tags from paralog match; Bit Score, E Values and Identities were obtained using the BLAST program with the redundant paralog against the Arabidopsis protein set from TIGR (The Institute for Genomic Research, ATH1 release 3.0). # indicates that these proteins are also members of the contaminant set outlined in Supplementary Table 3.